



## University of Groningen

### **A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology**

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**Supplementary Figure 1.** An example of some of the SBML annotations of compartments, species and reactions, using the example of the reaction catalyzed by the gene product hexokinase 2 of the *HXK2* gene, as used in the reconstruction of the consensus network, illustrating its use of the Systems Biology Ontology (<http://www.ebi.ac.uk/sbo/>) and its MIRIAM-compliance.

```
<?xml version="1.0" encoding="UTF-8"?>
<sbml xmlns="http://www.sbml.org/sbml/level2/version3" level="2"
version="3">
  <model metaid="metaid_ymn1_0" id="ymn1_0" name="Yeast metabolic network">
    <notes>
      <body xmlns="http://www.w3.org/1999/xhtml">
        <p>This is a reconstruction of the biochemical network of the yeast
          <i>Saccharomyces cerevisiae</i> carried out at a jamboree organized
in April 2007 in the Manchester Centre for Integrative Systems Biology. It
is the result of a consensus merger of two previous reconstructions.</p>
        <p>Technical notes:

          <ul>
            <li>The compartments included here have no volume defined; there
are no reliable estimates available for those volumes yet.</li>
            <li>There are no kinetic functions defined for the reactions
because this model only represents the chemical structure of the network
(stoichiometry).</li>
            <li>All reactions are marked reversible because all chemical
reactions are reversible.</li>
          </ul>
        </p>
        <p>This SBML representation of the yeast metabolic network is made
available under the Creative Commons Attribution-Share Alike 3.0 Unported
Licence (see
          <a
href="http://www.creativecommons.org">www.creativecommons.org</a>).</p>
      </body>
    </notes>
    <annotation>
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xmlns:dc="http://purl.org/dc/elements/1.1/"
xmlns:dcterms="http://purl.org/dc/terms/"
xmlns:vCard="http://www.w3.org/2001/vcard-rdf/3.0#"
xmlns:bqbiol="http://biomodels.net/biology-qualifiers/"
xmlns:bqmodel="http://biomodels.net/model-qualifiers/">
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          <dc:creator rdf:parseType="Resource">
            <rdf:Bag>
              <rdf:li rdf:parseType="Resource">
                <vCard:N rdf:parseType="Resource">
                  <vCard:Family>Herrgard</vCard:Family>
                  <vCard:Given>Markus</vCard:Given>
                </vCard:N>
                <vCard:EMAIL>mherrgar@ucsd.edu</vCard:EMAIL>
                <vCard:ORG>
                  <vCard:Orgname>University of California, San
Diego</vCard:Orgname>
                </vCard:ORG>
              </rdf:li>
              <rdf:li rdf:parseType="Resource">
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                  <vCard:Family>Swainston</vCard:Family>
```

```

        <vCard:Given>Neil</vCard:Given>
      </vCard:N>
      <vCard:EMAIL>neil.swainston@manchester.ac.uk</vCard:EMAIL>
      <vCard:ORG>
        <vCard:Orgname>University of Manchester</vCard:Orgname>
      </vCard:ORG>
    </rdf:li>
  </rdf:Bag>
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  <dcterms:W3CDTF>2008-05-15T17:52:27Z</dcterms:W3CDTF>
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  </rdf:Bag>
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</rdf:RDF>
</annotation>
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sboTerm="SBO:0000290">
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xmlns:dc="http://purl.org/dc/elements/1.1/"
xmlns:dcterms="http://purl.org/dc/terms/"
xmlns:vCard="http://www.w3.org/2001/vcard-rdf/3.0#"
xmlns:bqbiol="http://biomodels.net/biology-qualifiers/"
xmlns:bqmodel="http://biomodels.net/model-qualifiers/">
          <rdf:Description rdf:about="#metaid_C_4">
            <bqbiol:is>
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              </rdf:Bag>
            </bqbiol:is>
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    </compartment>
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</listOfSpecies>
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sboTerm="SBO:0000299">
    <annotation>
      <in:inchi xmlns:in="http://biomodels.net/inchi" metaid="M_172_inchi">
InChI=1/C10H16N5O13P3/c11-8-5-9(13-2-12-8)15(3-14-5)10-7(17)6
(16)4(26-10)1-25-30(21,22)28-31(23,24)27-29(18,19)20/h2-4,6-7,10,16-17H,1H2,
(H,21,22)(H,23,24)(H2,11,12,13)(H2,18,19,20)/t4-,6-,7-,10-/m1/s1/f/h18-19,21
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    <rdf:RDF xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#"

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xmlns:bqbiol="http://biomodels.net/biology-qualifiers/"
xmlns:bqmodel="http://biomodels.net/model-qualifiers/">
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      <rdf:Bag>
        <rdf:li rdf:resource="urn:miriam:obo.chebi:CHEBI:15422"/>
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      </rdf:Bag>
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  </rdf:Description>
</rdf:RDF>
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xmlns:dcterms="http://purl.org/dc/terms/"
xmlns:vCard="http://www.w3.org/2001/vcard-rdf/3.0#"
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xmlns:bqmodel="http://biomodels.net/model-qualifiers/">
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    </rdf:Description>
  </rdf:RDF>
</annotation>
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:
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</listOfReactions>
:
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(D-glucose:ATP)" sboTerm="SBO:0000176">
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        <p>SUBSYSTEM: Glycolysis/Gluconeogenesis</p>
      </html>
    </notes>
    <annotation>
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xmlns:dcterms="http://purl.org/dc/terms/"
xmlns:vCard="http://www.w3.org/2001/vcard-rdf/3.0#"
xmlns:bqbiol="http://biomodels.net/biology-qualifiers/"
xmlns:bqmodel="http://biomodels.net/model-qualifiers/">
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  </listOfReactions>
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</sbml>

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